

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: White, Mark Leslie
Carroll, Stephen Fitzhugh
Ma, Jeremy Kam-kuen
- (ii) TITLE OF INVENTION: METHOD FOR QUANTIFYING LBP IN BODY FLUIDS
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY INFORMATION:
 - (A) NAME: Lin-Laures, Li-Hsien
 - (B) REGISTRATION NUMBER: 33,547
 - (C) REFERENCE/DOCKET NUMBER: 27129/33783
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/474-6300
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1443
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 76..1443
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: "rLBP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GGG GCC TTG GCC AGA GCC CTG CCG TCC ATA CTG CTG GCA TTG CTG Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu -25 -20 -15 -10	48
CTT ACG TCC ACC CCA GAG GCT CTG GGT GCC AAC CCC GGC TTG GTC GCC Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala -5 1 5	96
AGG ATC ACC GAC AAG GGA CTG CAG TAT GCG GCC CAG GAG GGG CTA TTG Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu 10 15 20	144
GCT CTG CAG AGT GAG CTG CTC AGG ATC ACG CTG CCT GAC TTC ACC GGG Ala Leu Gln Ser Glu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly 25 30 35	192
GAC TTG AGG ATC CCC CAC GTC GGC CGT GGG CGC TAT GAG TTC CAC AGC Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser 40 45 50 55	240
CTG AAC ATC CAC AGC TGT GAG CTG CTT CAC TCT GCG CTG AGG CCT GTC Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val 60 65 70	288
CCT GGC CAG GGC CTG AGT CTC AGC ATC TCC GAC TCC TCC ATC CGG GTC Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val 75 80 85	336
CAG GGC AGG TGG AAG GTG CGC AAG TCA TTC TTC AAA CTA CAG GGC TCC Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser 90 95 100	384
TTT GAT GTC AGT GTC AAG GGC ATC AGC ATT TCG GTC AAC CTC CTG TTG Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu 105 110 115	432
GGC AGC GAG TCC TCC GGG AGG CCC ACA GTT ACT GCC TCC AGC TGC AGC Gly Ser Glu Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser 120 125 130 135	480
AGT GAC ATC GCT GAC GTG GAG GTG GAC ATG TCG GGA GAC TTG GGG TGG Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp 140 145 150	528
CTG TTG AAC CTC TTC CAC AAC CAG ATT GAG TCC AAG TTC CAG AAA GTA Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val 155 160 165	576
CTG GAG AGC AGG ATT TGC GAA ATG ATC CAG AAA TCG GTG TCC TCC GAT Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp 170 175 180	624
CTA CAG CCT TAT CTC CAA ACT CTG CCA GTT ACA ACA GAG ATT GAC AGT Leu Gln Pro Tyr Leu Gln Thr Leu Pro Val Thr Thr Glu Ile Asp Ser 185 190 195	672
TTC GCC GAC ATT GAT TAT AGC TTA GTG GAA GCC CCT CGG GCA ACA GCC Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala 200 205 210 215	720
CAG ATG CTG GAG GTG ATG TTT AAG GGT GAA ATC TTT CAT CGT AAC CAC Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His 220 225 230	768

CGT TCT CCA GTT ACC CTC CTT GCT GCA GTC ATG AGC CTT CCT GAG GAA	816
Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu	
235 240 245	
CAC AAC AAA ATG GTC TAC TTT GCC ATC TCG GAT TAT GTC TTC AAC ACG	864
His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr	
250 255 260	
GCC AGC CTG GTT TAT CAT GAG GAA GGA TAT CTG AAC TTC TCC ATC ACA	912
Ala Ser Leu Val Tyr His Glu Glu Gly Tyr Leu Asn Phe Ser Ile Thr	
265 270 275	
GAT GAG ATG ATA CCG CCT GAC TCT AAT ATC CGA CTG ACC ACC AAG TCC	960
Asp Glu Met Ile Pro Pro Asp Ser Asn Ile Arg Leu Thr Thr Lys Ser	
280 285 290 295	
TTC CGA CCC TTC GTC CCA CGG TTA GCC AGG CTC TAC CCC AAC ATG AAC	1008
Phe Arg Pro Phe Val Pro Arg Leu Ala Arg Leu Tyr Pro Asn Met Asn	
300 305 310	
CTG GAA CTC CAG GGA TCA GTG CCC TCT GCT CCG CTC CTG AAC TTC AGC	1056
Leu Glu Leu Gln Gly Ser Val Pro Ser Ala Pro Leu Leu Asn Phe Ser	
315 320 325	
CCT GGG AAT CTG TCT GTG GAC CCC TAT ATG GAG ATA GAT GCC TTT GTG	1104
Pro Gly Asn Leu Ser Val Asp Pro Tyr Met Glu Ile Asp Ala Phe Val	
330 335 340	
CTC CTG CCC AGC TCC AGC AAG GAG CCT GTC TTC CGG CTC AGT GTG GCC	1152
Leu Leu Pro Ser Ser Ser Lys Glu Pro Val Phe Arg Leu Ser Val Ala	
345 350 355	
ACT AAT GTG TCC GCC ACC TTG ACC TTC AAT ACC AGC AAG ATC ACT GGG	1200
Thr Asn Val Ser Ala Thr Leu Thr Phe Asn Thr Ser Lys Ile Thr Gly	
360 365 370 375	
TTC CTG AAG CCA GGA AAG GTA AAA GTG GAA CTG AAA GAA TCC AAA GTT	1248
Phe Leu Lys Pro Gly Lys Val Lys Val Glu Leu Lys Glu Ser Lys Val	
380 385 390	
GGA CTA TTC AAT GCA GAG CTG TTG GAA GCG CTC CTC AAC TAT TAC ATC	1296
Gly Leu Phe Asn Ala Glu Leu Leu Glu Ala Leu Leu Asn Tyr Tyr Ile	
395 400 405	
CTT AAC ACC TTC TAC CCC AAG TTC AAT GAT AAG TTG GCC GAA GGC TTC	1344
Leu Asn Thr Phe Tyr Pro Lys Phe Asn Asp Lys Leu Ala Glu Gly Phe	
410 415 420	
CCC CTT CCT CTG CTG AAG CGT GTT CAG CTC TAC GAC CTT GGG CTG CAG	1392
Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu Gly Leu Gln	
425 430 435	
ATC CAT AAG GAC TTC CTG TTC TTG GGT GCC AAT GTC CAA TAC ATG AGA	1440
Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln Tyr Met Arg	
440 445 450 455	
GTT	1443
Val	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "rLBP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu
-25                -20                -15                -10

Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala
          -5                      1                      5

Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu
      10                15                20

Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly
  25                30                35

Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser
  40                45                50                55

Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val
          60                65                70

Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val
      75                80                85

Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser
  90                95                100

Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu
 105                110                115

Gly Ser Glu Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser
 120                125                130                135

Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp
          140                145                150

Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val
 155                160                165

Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp
 170                175                180

Leu Gln Pro Tyr Leu Gln Thr Leu Pro Val Thr Thr Glu Ile Asp Ser
 185                190                195

Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala
 200                205                210                215

Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His
 220                225                230

Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu
 235                240                245

His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr
 250                255                260

Ala Ser Leu Val Tyr His Glu Glu Gly Tyr Leu Asn Phe Ser Ile Thr
 265                270                275

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Asp Glu Met Ile Pro Pro Asp Ser Asn Ile Arg Leu Thr Thr Lys Ser
 280 285 290 295
 Phe Arg Pro Phe Val Pro Arg Leu Ala Arg Leu Tyr Pro Asn Met Asn
 300 305 310
 Leu Glu Leu Gln Gly Ser Val Pro Ser Ala Pro Leu Leu Asn Phe Ser
 315 320 325
 Pro Gly Asn Leu Ser Val Asp Pro Tyr Met Glu Ile Asp Ala Phe Val
 330 335 340
 Leu Leu Pro Ser Ser Ser Lys Glu Pro Val Phe Arg Leu Ser Val Ala
 345 350 355
 Thr Asn Val Ser Ala Thr Leu Thr Phe Asn Thr Ser Lys Ile Thr Gly
 360 365 370 375
 Phe Leu Lys Pro Gly Lys Val Lys Val Glu Leu Lys Glu Ser Lys Val
 380 385 390
 Gly Leu Phe Asn Ala Glu Leu Leu Glu Ala Leu Leu Asn Tyr Tyr Ile
 395 400 405
 Leu Asn Thr Phe Tyr Pro Lys Phe Asn Asp Lys Leu Ala Glu Gly Phe
 410 415 420
 Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu Gly Leu Gln
 425 430 435
 Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln Tyr Met Arg
 440 445 450 455
 Val

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..591

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "rLBP25"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCC AAC CCC GGC TTG GTC GCC AGG ATC ACC GAC AAG GGA CTG CAG TAT	48
Ala Asn Pro Gly Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr	
1 5 10 15	
GCG GCC CAG GAG GGG CTA TTG GCT CTG CAG AGT GAG CTG CTC AGG ATC	96
Ala Ala Gln Glu Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile	
20 25 30	
ACG CTG CCT GAC TTC ACC GGG GAC TTG AGG ATC CCC CAC GTC GGC CGT	144
Thr Leu Pro Asp Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg	

35	40	45	
GGG CGC TAT GAG TTC CAC AGC CTG AAC ATC CAC AGC TGT GAG CTG CTT Gly Arg Tyr Glu Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu 50 55 60			192
CAC TCT GCG CTG AGG CCT GTC CCT GGC CAG GGC CTG AGT CTC AGC ATC His Ser Ala Leu Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile 65 70 75 80			240
TCC GAC TCC TCC ATC CGG GTC CAG GGC AGG TGG AAG GTG CGC AAG TCA Ser Asp Ser Ser Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser 85 90 95			288
TTC TTC AAA CTA CAG GGC TCC TTT GAT GTC AGT GTC AAG GGC ATC AGC Phe Phe Lys Leu Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser 100 105 110			336
ATT TCG GTC AAC CTC CTG TTG GGC AGC GAG TCC TCC GGG AGG CCC ACA Ile Ser Val Asn Leu Leu Leu Gly Ser Glu Ser Ser Gly Arg Pro Thr 115 120 125			384
GTT ACT GCC TCC AGC TGC AGC AGT GAC ATC GCT GAC GTG GAG GTG GAC Val Thr Ala Ser Ser Cys Ser Ser Asp Ile Ala Asp Val Glu Val Asp 130 135 140			432
ATG TCG GGA GAC TTG GGG TGG CTG TTG AAC CTC TTC CAC AAC CAG ATT Met Ser Gly Asp Leu Gly Trp Leu Leu Asn Leu Phe His Asn Gln Ile 145 150 155 160			480
GAG TCC AAG TTC CAG AAA GTA CTG GAG AGC AGG ATT TGC GAA ATG ATC Glu Ser Lys Phe Gln Lys Val Leu Glu Ser Arg Ile Cys Glu Met Ile 165 170 175			528
CAG AAA TCG GTG TCC TCC GAT CTA CAG CCT TAT CTC CAA ACT CTG CCA Gln Lys Ser Val Ser Ser Asp Leu Gln Pro Tyr Leu Gln Thr Leu Pro 180 185 190			576
GTT ACA ACA GAG ATT Val Thr Thr Glu Ile 195			591

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "rLBP25"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Asn Pro Gly Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr 1 5 10 15
Ala Ala Gln Glu Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile 20 25 30
Thr Leu Pro Asp Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg

35					40					45					
Gly	Arg	Tyr	Glu	Phe	His	Ser	Leu	Asn	Ile	His	Ser	Cys	Glu	Leu	Leu
	50					55					60				
His	Ser	Ala	Leu	Arg	Pro	Val	Pro	Gly	Gln	Gly	Leu	Ser	Leu	Ser	Ile
65						70					75				80
Ser	Asp	Ser	Ser	Ile	Arg	Val	Gln	Gly	Arg	Trp	Lys	Val	Arg	Lys	Ser
				85					90					95	
Phe	Phe	Lys	Leu	Gln	Gly	Ser	Phe	Asp	Val	Ser	Val	Lys	Gly	Ile	Ser
			100					105					110		
Ile	Ser	Val	Asn	Leu	Leu	Leu	Gly	Ser	Glu	Ser	Ser	Gly	Arg	Pro	Thr
		115					120					125			
Val	Thr	Ala	Ser	Ser	Cys	Ser	Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp
	130					135					140				
Met	Ser	Gly	Asp	Leu	Gly	Trp	Leu	Leu	Asn	Leu	Phe	His	Asn	Gln	Ile
145					150					155					160
Glu	Ser	Lys	Phe	Gln	Lys	Val	Leu	Glu	Ser	Arg	Ile	Cys	Glu	Met	Ile
				165					170					175	
Gln	Lys	Ser	Val	Ser	Ser	Asp	Leu	Gln	Pro	Tyr	Leu	Gln	Thr	Leu	Pro
			180					185					190		
Val	Thr	Thr	Glu	Ile											
			195												